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RAW SEQUENCE LISTING

DATE: 04/23/2002

PATENT APPLICATION: US/10/077,698

TIME: 11:02:07

Input Set : N:\Crf3\RULE60\10077698.raw

Output Set: N:\CRF3\04232002\J077698.raw

1 <110> APPLICANT: Glucksmann, Maria A.
 2 <120> TITLE OF INVENTION: 14273 Receptor, A Novel G-Protein Coupled Receptor
 3 <130> FILE REFERENCE: 5800-4B, 035800/177086
 4 <140> CURRENT APPLICATION NUMBER: 10/077,698
 5 <141> CURRENT FILING DATE: 2002-02-13
 6 <150> PRIOR APPLICATION NUMBER: 09/261,599
 7 <151> PRIOR FILING DATE: 1999-02-26
 10 <150> PRIOR APPLICATION NUMBER: 09/107,761
 11 <151> PRIOR FILING DATE: 1998-06-30
 12 <150> PRIOR APPLICATION NUMBER: 09/223,538
 13 <151> PRIOR FILING DATE: 1998-12-30
 14 <160> NUMBER OF SEQ ID NOS: 7
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 361
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
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 26 Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
 27 35 40 45
 28 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 29 50 55 60
 30 Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
 31 65 70 75 80
 32 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
 33 85 90 95
 34 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 35 100 105 110
 36 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 37 115 120 125
 38 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 39 130 135 140
 40 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
 41 145 150 155 160
 42 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
 43 165 170 175
 44 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
 45 180 185 190
 46 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp

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49          210          215          220
50 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
51          225          230          235          240
52 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
53          245          250          255
54 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
55          260          265          270
56 Phe Phe Ile Met Trp Ser Pro Ile Ile Thr Ile Leu Leu Ile Leu
57          275          280          285
58 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
59          290          295          300
60 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
61          305          310          315          320
62 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
63          325          330          335
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71 <212> TYPE: DNA
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76 cttcttctcc gacgtcaagg gcgaccaccg gctggtgctg gccgcggtgg agacaaccgt 180
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78 gcgcgcagca cgccgcggcg cgaactgcct cctggtactc aacctcttct gcgcggacct 300
79 gctcttcate agcgtatccc ctctggtgct ggccgtgcgc tggactgagg cctggctgct 360
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81 cctcacgctg gccgcggtca gcctggagcg catggtgtgc atcgtgcacc tgcagcgcgg 480
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84 cgccgaccag gaaatttcga ttgcacact gatttggccc accattcctg gagagatctc 660
85 gtgggatgtc tcttttgtaa cttgaactt cttggtgcc aagactcctc ttgtgatcag 720
86 ttactccaaa attttacaga tcacaaagcg atcaaggaa aggctcacgg taagcctggc 780
87 ctactcggag agccaccaga tcgcgtgtc ccagcaggac ttccggctct tccgcacct 840
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89 catcctgato cagaacttca agcaagacct ggtcatctgg ccgtccctct tctctgggt 960
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91 caggaatgag tggaaagaaa ttttttgctg cttctggttc ccagaaaagg gagccatttt 1080
92 aacagacaca tctgtcaaaa gaaatgactt gtcgattatt ttggctaat ttttctttat 1140
93 agccgagttt ctacacactg gcgagctgtg gcatgctttt aaacagagtt catttccagt 1200
94 accctccatc agtgaccctt gctttaagaa aatgaaccta tgcaaataga catccacagc 1260
95 gtcggtaaat taagggttga tcaccaagtt tcataatatt ttccctttat aaaaggattt 1320
96 gttggccagg tgcagtgggt catgcctgta atcccagcag ttggggaggg tgagggtgggt 1380

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98      tactaaaaat aaaaaaaaaa attagctggg agtgggtggtg ggcacctgta atcctagcta 1500
99      cttggggaggc tgaaccagga gaatctcttg aacctgggag gcagagggtg cagtgaagccg 1560
100     agatcgtgcc attgcactcc aaccagggca acaagagtga aactccatct taaaaaaaaa 1620
101     aaaaaaaaaa tttgttatgg gttcctttta aatgtgaact tttttagtgt gtttgtaata 1680
102     tgatcaaatt taataaatat ttatttatga ctgttcagca aaaaaaaaaa aaaaaaaagg 1740
103     cgg                                     1743
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106 <211> LENGTH: 259
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108 <213> ORGANISM: Unknown
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Unknown Organism: Seven
111      Transmembrane Segment Rhodopsin Superfamily
112 <400> SEQUENCE: 3
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115      Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
116      20          25          30
117      Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
118      35          40          45
119      Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
120      50          55          60
121      Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Thr Ala Ile
122      65          70          75          80
123      Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
124      85          90          95
125      Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
126      100         105         110
127      Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
128      115         120         125
129      Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130      130         135         140
131      Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
132      145         150         155         160
133      Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
134      165         170         175
135      Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
136      180         185         190
137      Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Phe Val Leu Cys
138      195         200         205
139      Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
140      210         215         220
141      Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
142      225         230         235         240
143      Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
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145      Ile Ile Tyr
147 <210> SEQ ID NO: 4

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148 <211> LENGTH: 361
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150 <213> ORGANISM: Murine ortholog
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154 Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
155 20 25 30
156 Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
157 35 40 45
158 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
159 50 55 60
160 Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn
161 65 70 75 80
162 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
163 85 90 95
164 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
165 100 105 110
166 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
167 115 120 125
168 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
169 130 135 140
170 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
171 145 150 155 160
172 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu
173 165 170 175
174 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
175 180 185 190
176 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
177 195 200 205
178 Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
179 210 215 220
180 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
181 225 230 235 240
182 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
183 245 250 255
184 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
185 260 265 270
186 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
187 275 280 285
188 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
189 290 295 300
190 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
191 305 310 315 320
192 Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
193 325 330 335
194 Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
195 340 345 350
196 Arg Asn Asp Leu Ser Val Ile Ser Ser

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Input Set : N:\Crf3\RULE60\10077698.raw

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197          355          360
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202 <213> ORGANISM: Murine ortholog
203 <400> SEQUENCE: 5
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206      tcgatgaccc tcttgacagc cagcagcgcg cgcagctccg ccattctccc ggacgcgtgg 180
207      gcggggcgcc cgcatgtccc cctgagtgtg cacagacgac gggccctggt cctcgcaca 240
208      cccctgaacca agtcaatcgc acccaattcc ctctcttctc ggatgtcaag ggcgaccacc 300
209      ggttggtggt gagcgtcgtg gagaccaccg ttctgggact catctttgtc gtctcactgc 360
210      tgggcaacgt gtgtgtctta gtgctggtgg cgcgcgctcg gcgcgctggg gcgtcagcca 420
211      gcctggtgct caacctcttc tgcgcggatt tgctcttcac cagcgccatc cctctagtgc 480
212      tcgtcgtgct ctggactgag gcctggctgt tggggcccgt cgtctgccac ctgctcttct 540
213      acgtgatgac aatgagcggc agcgtcacga tctcacact ggccgcggtc agcctggagc 600
214      gcatggtgtg catcgtgcgc ctccggcgcg gcttgagcgg cccggggcgg cggactcagg 660
215      cggcactgct ggctttcata tggggttact cggcgctcgc cgcgtgccc ctctacatct 720
216      tgttccgcgt ggtcccgcag cgccttcccg gcggggacca ggaattccg atttgcacat 780
217      tggattggcc caaccgcata ggagaaatct catgggatgt gttttttgag accttgaact 840
218      tcttggtgcc gggactgtgc atttgtatca gttactccaa aattttacag atcacgaaag 900
219      catcgcggaa gaggcttacg ctgagcttgg catactctga gagccaccag atccgagtgt 960
220      cccaacaaga ctaccgaact tccgcacgct tcttctgct catggtttcc ttcttcatca 1020
221      tgtggagtcc catcatcatc accatctccc tcatcttgat ccaaaaacttc cggcaggacc 1080
222      tggtcactcg gccatccctt ttcttctggg tggtgccett cacgtttgcc aactctgccc 1140
223      taaaccccat actgtacaac atgtcgtgt tcaggaaaga atggaggaag attttttgct 1200
224      gcttcttttt tccagagaag ggagccattt ttacagatac gtctgtcagg cgaaatgact 1260
225      tgtctgttat ttccagctaa ctagcctctg gtgccagggt aaccacggtg tgcatgtaaa 1320
226      gggagttaac ttcaaggaaa gccaccagt gcgccctgct taaaaaatac ccgacttcca 1380
227      acagcaggca tctacggagc cagcaaatta aggaatgatc gtcagtata aaaatatttt 1440
228      tctttaaag aactttctat gggttccttt tgtgaacttt ttaagtgtg ttgtaatat 1500
229      gatctagtta ataaattttt atttataacg tgttctaca aaaaaaaaaa aaaaaaaaaa 1560
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232 <211> LENGTH: 300
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <223> OTHER INFORMATION: mature polypeptide of 14273
237 <400> SEQUENCE: 6
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241      20          25          30
242      Leu Val Leu Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val
243      35          40          45
244      Ala Cys His Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr
245      50          55          60
246      Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val
247      65          70          75          80

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/077,698

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